



SEQUENCE LISTING

<110> Hui-Quan Kwak, Keith

<120> Human E3 Alpha Ubiquitin Ligase Family

<130> 01017/35966A

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<141> 2000-11-28

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<160> 29

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<210> 1

<211> 6308

<212> DNA

<213> Homo sapiens

<220>

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gctgattcaa aattatggaa aacttttctga gggctgggaa agtattggag ggtcttttgc 6052

tccatgtcca gggttcaactta catcaataaa atatttctta atggagtatt gctttcaatt 6112

agcaaacata tgcttcacag gaaaaaagga catagatcaa tctgttttat gtgctagtat 6172

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 Val Asp Phe Tyr Thr Ala Phe Leu His His Leu Ala Gln Leu Val Pro
 35 40 45
 Glu Ile Tyr Phe Ala Glu Met Asp Pro Asp Leu Glu Lys Gln Glu Glu
 50 55 60
 Ser Val Gln Met Ser Ile Phe Thr Pro Leu Glu Trp Tyr Leu Phe Gly
 65 70 75 80
 Glu Asp Pro Asp Ile Cys Leu Glu Lys Leu Lys His Ser Gly Ala Phe
 85 90 95
 Gln Leu Cys Gly Arg Val Phe Lys Ser Gly Glu Thr Thr Tyr Ser Cys
 100 105 110

Arg	Asp	Cys	Ala	Ile	Asp	Pro	Thr	Cys	Val	Leu	Cys	Met	Asp	Cys	Phe	115	120	125
Gln	Asp	Ser	Val	His	Lys	Asn	His	Arg	Tyr	Lys	Met	His	Thr	Ser	Thr	130	135	140
Gly	Gly	Gly	Phe	Cys	Asp	Cys	Gly	Asp	Thr	Glu	Ala	Trp	Lys	Thr	Gly	145	150	155
Pro	Phe	Cys	Val	Asn	His	Glu	Pro	Gly	Arg	Ala	Gly	Thr	Ile	Lys	Glu	165	170	175
Asn	Ser	Arg	Cys	Pro	Leu	Asn	Glu	Glu	Val	Ile	Val	Gln	Ala	Arg	Lys	180	185	190
Ile	Phe	Pro	Ser	Val	Ile	Lys	Tyr	Val	Val	Glu	Met	Thr	Ile	Trp	Glu	195	200	205
Glu	Glu	Lys	Glu	Leu	Pro	Pro	Glu	Leu	Gln	Ile	Arg	Glu	Lys	Asn	Glu	210	215	220
Arg	Tyr	Tyr	Cys	Val	Leu	Phe	Asn	Asp	Glu	His	His	Ser	Tyr	Asp	His	225	230	235
Val	Ile	Tyr	Ser	Leu	Gln	Arg	Ala	Leu	Asp	Cys	Glu	Leu	Ala	Glu	Ala	245	250	255
Gln	Leu	His	Thr	Thr	Ala	Ile	Asp	Lys	Glu	Gly	Arg	Arg	Ala	Val	Lys	260	265	270
Ala	Gly	Ala	Tyr	Ala	Ala	Cys	Gln	Glu	Ala	Lys	Glu	Asp	Ile	Lys	Ser	275	280	285
His	Ser	Glu	Asn	Val	Ser	Gln	His	Pro	Leu	His	Val	Glu	Val	Leu	His	290	295	300
Ser	Glu	Ile	Met	Ala	His	Gln	Lys	Phe	Ala	Leu	Arg	Leu	Gly	Ser	Trp	305	310	315
Met	Asn	Lys	Ile	Met	Ser	Tyr	Ser	Ser	Asp	Phe	Arg	Gln	Ile	Phe	Cys	325	330	335
Gln	Ala	Cys	Leu	Arg	Glu	Glu	Pro	Asp	Ser	Glu	Asn	Pro	Cys	Leu	Ile	340	345	350
Ser	Arg	Leu	Met	Leu	Trp	Asp	Ala	Lys	Leu	Tyr	Lys	Gly	Ala	Arg	Lys	355	360	365
Ile	Leu	His	Glu	Leu	Ile	Phe	Ser	Ser	Phe	Phe	Met	Glu	Met	Glu	Tyr	370	375	380
Lys	Lys	Leu	Phe	Ala	Met	Glu	Phe	Val	Lys	Tyr	Tyr	Lys	Gln	Leu	Gln	385	390	395
Lys	Glu	Tyr	Ile	Ser	Asp	Asp	His	Asp	Arg	Ser	Ile	Ser	Ile	Thr	Ala	405	410	415
Leu	Ser	Val	Gln	Met	Phe	Thr	Val	Pro	Thr	Leu	Ala	Arg	His	Leu	Ile	420	425	430
Glu	Glu	Gln	Asn	Val	Ile	Ser	Val	Ile	Thr	Glu	Thr	Leu	Leu	Glu	Val	435	440	445

Leu Pro Glu Tyr Leu Asp Arg Asn Asn Lys Phe Asn Phe Gln Gly Tyr
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 Ser Gln Asp Lys Leu Gly Arg Val Tyr Ala Val Ile Cys Asp Leu Lys
 465 470 475 480
 Tyr Ile Leu Ile Ser Lys Pro Thr Ile Trp Thr Glu Arg Leu Arg Met
 485 490 495
 Gln Phe Leu Glu Gly Phe Arg Ser Phe Leu Lys Ile Leu Thr Cys Met
 500 505 510
 Gln Gly Met Glu Glu Ile Arg Arg Gln Val Gly Gln His Ile Glu Val
 515 520 525
 Asp Pro Asp Trp Glu Ala Ala Ile Ala Ile Gln Met Gln Leu Lys Asn
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 Ile Leu Leu Met Phe Gln Glu Trp Cys Ala Cys Asp Glu Glu Leu Leu
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 Ser Phe Ile Ser Ser Ser Lys Thr Val Val Gln Ser Cys Gly His Ser
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 Leu Glu Thr Lys Ser Tyr Arg Val Ser Glu Asp Leu Val Ser Ile His
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 Gln Val Glu Val Leu Val Glu Tyr Pro Leu Arg Cys Leu Val Leu Val
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 Ser Gln Val Phe Tyr Tyr Gln Asp Val Lys Cys Arg Glu Glu Met Tyr
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 Asp Lys Asp Ile Ile Met Leu Gln Ile Gly Ala Ser Leu Met Asp Pro
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 Asn Lys Phe Leu Leu Leu Val Leu Gln Arg Tyr Glu Leu Ala Glu Ala
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 725 730 735
 Asn Thr Leu Ile Glu Glu Met Leu Gln Val Leu Ile Tyr Ile Val Gly
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 Glu Arg Tyr Val Pro Gly Val Gly Asn Val Thr Lys Glu Glu Val Thr
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Met Arg Glu Ile Ile His Leu Leu Cys Ile Glu Pro Met Pro His Ser
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 Gly His Gly Val Tyr Glu Leu Lys Asp Glu Ser Leu Lys Asp Phe Asn
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 835 840 845
 Met Gln Lys Lys Arg Arg Lys Gln Glu Asn Lys Asp Glu Ala Leu Pro
 850 855 860
 Pro Pro Pro Pro Pro Glu Phe Cys Pro Ala Phe Ser Lys Val Ile Asn
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 Lys Leu Lys Gly Ile Pro Gln Leu Glu Gly Gln Lys Asp Met Ile Thr
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 995 1000 1005
 Glu Ile Thr His Asp Lys Glu Lys Ala Glu Arg Lys Arg Lys Ala
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 1055 1060 1065
 Glu Ser Thr Pro Ala Val Ser Asp Tyr Ser Arg Ile Ala Leu Gly
 1070 1075 1080
 Pro Lys Arg Gly Pro Ser Val Thr Glu Lys Glu Val Leu Thr Cys
 1085 1090 1095

Ile	Leu	Cys	Gln	Glu	Glu	Gln	Glu	Val	Lys	Ile	Glu	Asn	Asn	Ala
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Met	Val	Leu	Ser	Ala	Cys	Val	Gln	Lys	Ser	Thr	Ala	Leu	Thr	Gln
1115						1120					1125			
His	Arg	Gly	Lys	Pro	Ile	Glu	Leu	Ser	Gly	Glu	Ala	Leu	Asp	Pro
1130						1135					1140			
Leu	Phe	Met	Asp	Pro	Asp	Leu	Ala	Tyr	Gly	Thr	Tyr	Thr	Gly	Ser
1145						1150					1155			
Cys	Gly	His	Val	Met	His	Ala	Val	Cys	Trp	Gln	Lys	Tyr	Phe	Glu
1160						1165					1170			
Ala	Val	Gln	Leu	Ser	Ser	Gln	Gln	Arg	Ile	His	Val	Asp	Leu	Phe
1175						1180					1185			
Asp	Leu	Glu	Ser	Gly	Glu	Tyr	Leu	Cys	Pro	Leu	Cys	Lys	Ser	Leu
1190						1195					1200			
Cys	Asn	Thr	Val	Ile	Pro	Ile	Ile	Pro	Leu	Gln	Pro	Gln	Lys	Ile
1205						1210					1215			
Asn	Ser	Glu	Asn	Ala	Asp	Ala	Leu	Ala	Gln	Leu	Leu	Thr	Leu	Ala
1220						1225					1230			
Arg	Trp	Ile	Gln	Thr	Val	Leu	Ala	Arg	Ile	Ser	Gly	Tyr	Asn	Ile
1235						1240					1245			
Arg	His	Ala	Lys	Gly	Glu	Asn	Pro	Ile	Pro	Ile	Phe	Phe	Asn	Gln
1250						1255					1260			
Gly	Met	Gly	Asp	Ser	Thr	Leu	Glu	Phe	His	Ser	Ile	Leu	Ser	Phe
1265						1270					1275			
Gly	Val	Glu	Ser	Ser	Ile	Lys	Tyr	Ser	Asn	Ser	Ile	Lys	Glu	Met
1280						1285					1290			
Val	Ile	Leu	Phe	Ala	Thr	Thr	Ile	Tyr	Arg	Ile	Gly	Leu	Lys	Val
1295						1300					1305			
Pro	Pro	Asp	Glu	Arg	Asp	Pro	Arg	Val	Pro	Met	Leu	Thr	Trp	Ser
1310						1315					1320			
Thr	Cys	Ala	Phe	Thr	Ile	Gln	Ala	Ile	Glu	Asn	Leu	Leu	Gly	Asp
1325						1330					1335			
Glu	Gly	Lys	Pro	Leu	Phe	Gly	Ala	Leu	Gln	Asn	Arg	Gln	His	Asn
1340						1345					1350			
Gly	Leu	Lys	Ala	Leu	Met	Gln	Phe	Ala	Val	Ala	Gln	Arg	Ile	Thr
1355						1360					1365			
Cys	Pro	Gln	Val	Leu	Ile	Gln	Lys	His	Leu	Val	Arg	Leu	Leu	Ser
1370						1375					1380			
Val	Val	Leu	Pro	Asn	Ile	Lys	Ser	Glu	Asp	Thr	Pro	Cys	Leu	Leu
1385						1390					1395			
Ser	Ile	Asp	Leu	Phe	His	Val	Leu	Val	Gly	Ala	Val	Leu	Ala	Phe
1400						1405					1410			

Pro	Ser	Leu	Tyr	Trp	Asp	Asp	Pro	Val	Asp	Leu	Gln	Pro	Ser	Ser
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Val	Ser	Ser	Ser	Tyr	Asn	His	Leu	Tyr	Leu	Phe	His	Leu	Ile	Thr
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Met	Ala	His	Met	Leu	Gln	Ile	Leu	Leu	Thr	Val	Asp	Thr	Gly	Leu
	1445					1450					1455			
Pro	Leu	Ala	Gln	Val	Gln	Glu	Asp	Ser	Glu	Glu	Ala	His	Ser	Ala
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Ser	Ser	Phe	Phe	Ala	Glu	Ile	Ser	Gln	Tyr	Thr	Ser	Gly	Ser	Ile
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Gly	Cys	Asp	Ile	Pro	Gly	Trp	Tyr	Leu	Trp	Val	Ser	Leu	Lys	Asn
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Gly	Ile	Thr	Pro	Tyr	Leu	Arg	Cys	Ala	Ala	Leu	Phe	Phe	His	Tyr
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Leu	Leu	Gly	Val	Thr	Pro	Pro	Glu	Glu	Leu	His	Thr	Asn	Ser	Ala
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Glu	Gly	Glu	Tyr	Ser	Ala	Leu	Cys	Ser	Tyr	Leu	Ser	Leu	Pro	Thr
	1535					1540					1545			
Asn	Leu	Phe	Leu	Leu	Phe	Gln	Glu	Tyr	Trp	Asp	Thr	Val	Arg	Pro
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Leu	Leu	Gln	Arg	Trp	Cys	Ala	Asp	Pro	Ala	Leu	Leu	Asn	Cys	Leu
	1565					1570					1575			
Lys	Gln	Lys	Asn	Thr	Val	Val	Arg	Tyr	Pro	Arg	Lys	Arg	Asn	Ser
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Ser	His	Phe	Arg	Cys	Pro	Arg	Ser	Ala	Asp	Asp	Glu	Arg	Lys	His
	1610					1615					1620			
Pro	Val	Leu	Cys	Leu	Phe	Cys	Gly	Ala	Ile	Leu	Cys	Ser	Gln	Asn
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	1655					1660					1665			
Lys	Ile	Arg	Glu	Cys	Arg	Val	Val	Leu	Val	Glu	Gly	Lys	Ala	Arg
	1670					1675					1680			
Gly	Cys	Ala	Tyr	Pro	Ala	Pro	Tyr	Leu	Asp	Glu	Tyr	Gly	Glu	Thr
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Arg Tyr Arg Lys Leu His Leu Val Trp Gln Gln His Cys Ile Ile
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Met
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Glu Cys Ser Ala Glu Glu Ile Ala Gly Lys Trp Leu Gln Ala Thr Asp
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Leu Thr Arg Glu Val Tyr Gln His Leu Ala His Tyr Val Pro Lys Ile
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Tyr Cys Arg Gly Pro Asn Pro Phe Pro Gln Lys Glu Asp Met Leu Ala
50 55 60 65
cag cat gtt ttg ttg gga cca atg gaa tgg tac ctt tgt ggt gaa gat 537
Gln His Val Leu Leu Gly Pro Met Glu Trp Tyr Leu Cys Gly Glu Asp
70 75 80
cct gca ttt gga ttt cca aaa ctt gag caa gca aac aaa cct tct cat 585
Pro Ala Phe Gly Phe Pro Lys Leu Glu Gln Ala Asn Lys Pro Ser His
85 90 95
ctt tgt ggt cgt gtt ttt aaa gta gga gag cct aca tat tct tgc aga 633
Leu Cys Gly Arg Val Phe Lys Val Gly Glu Pro Thr Tyr Ser Cys Arg
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gac tgt gca gtt gat cca act tgt gtt ttg tgc atg gag tgc ttt ttg 681
Asp Cys Ala Val Asp Pro Thr Cys Val Leu Cys Met Glu Cys Phe Leu
115 120 125

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Glu Leu Ser Pro Pro Met Leu Ile Glu His Pro Leu Arg Cys Leu Val	
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Gln Ile Phe Ser Thr Pro Asp Tyr Gly Lys Arg Phe Ser Ser Glu Ile	
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Gly Gln Val Asn Ala Thr Asp Glu Ile Lys Arg Glu Ile Ile His Gln	
770 775 780 785	
ttg agt atc aag cct atg gct cat agt gaa ttg gta aag tct tta cct	2697
Leu Ser Ile Lys Pro Met Ala His Ser Glu Leu Val Lys Ser Leu Pro	
790 795 800	
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Ala His Phe Lys Lys Pro Gly Leu Thr Gly Arg Gly Met Tyr Glu Leu	
820 825 830	
aaa cca gaa tgt gcc aaa gag ttc aac ttg tat ttc tat cac ttt tca	2841
Lys Pro Glu Cys Ala Lys Glu Phe Asn Leu Tyr Phe Tyr His Phe Ser	
835 840 845	
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Arg Ala Glu Gln Ser Lys Ala Glu Glu Ala Gln Arg Lys Leu Lys Arg	
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gcg cca aaa aat tct cct agc ata cta gct atg ctg gaa aca cta caa Ala Pro Lys Asn Ser Pro Ser Ile Leu Ala Met Leu Glu Thr Leu Gln 965 970 975	3225
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ccc gtg gca gag aca gaa gga acc ata atg gaa gag agt tca agg Pro Val Ala Glu Thr Glu Gly Thr Ile Met Glu Glu Ser Ser Arg 1010 1015 1020	3366
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caa Gln 1115	gaa Glu	gtt Val	aaa Lys	gtg Val	gaa Glu 1120	agc Ser	agg Arg	gca Ala	atg Met	gtc Val 1125	ttg Leu	gca Ala	gca Ala	ttt Phe	3681
gtt Val 1130	cag Gln	aga Arg	tca Ser	act Thr	gta Val 1135	tta Leu	tca Ser	aaa Lys	aac Asn	aga Arg 1140	agt Ser	aaa Lys	ttt Phe	att Ile	3726
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agt Ser 1265	act Thr	cct Pro	aat Asn	aat Asn	gcc Ala 1270	tct Ser	aca Thr	aag Lys	aat Asn	tca Ser 1275	gaa Glu	aat Asn	gtg Val	gat Asp	4131
gaa Glu 1280	tta Leu	cag Gln	ctc Leu	cct Pro	gaa Glu 1285	ggg Gly	ttc Phe	agg Arg	cct Pro	gat Asp 1290	ttt Phe	cgt Arg	cct Pro	aag Lys	4176
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 agaaaaatta g 6300

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 <213> Homo sapiens

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 Asp Leu Thr Arg Glu Val Tyr Gln His Leu Ala His Tyr Val Pro Lys
 35 40 45
 Ile Tyr Cys Arg Gly Pro Asn Pro Phe Pro Gln Lys Glu Asp Met Leu
 50 55 60
 Ala Gln His Val Leu Leu Gly Pro Met Glu Trp Tyr Leu Cys Gly Glu
 65 70 75 80
 Asp Pro Ala Phe Gly Phe Pro Lys Leu Glu Gln Ala Asn Lys Pro Ser
 85 90 95
 His Leu Cys Gly Arg Val Phe Lys Val Gly Glu Pro Thr Tyr Ser Cys
 100 105 110
 Arg Asp Cys Ala Val Asp Pro Thr Cys Val Leu Cys Met Glu Cys Phe
 115 120 125
 Leu Gly Ser Ile His Arg Asp His Arg Tyr Arg Met Thr Thr Ser Gly
 130 135 140
 Gly Gly Gly Phe Cys Asp Cys Gly Asp Thr Glu Ala Trp Lys Glu Gly
 145 150 155 160
 Pro Tyr Cys Gln Lys His Glu Leu Asn Thr Ser Glu Ile Glu Glu Glu
 165 170 175
 Glu Asp Pro Leu Val His Leu Ser Glu Asp Val Ile Ala Arg Thr Tyr
 180 185 190

Asn	Ile	Phe	Ala	Ile	Thr	Phe	Arg	Tyr	Ala	Val	Glu	Ile	Leu	Thr	Trp
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Asp	Thr	Tyr	Tyr	Cys	Met	Leu	Phe	Asn	Asp	Glu	Val	His	Thr	Tyr	Glu
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Gln	Val	Ile	Tyr	Thr	Leu	Gln	Lys	Ala	Val	Asn	Cys	Thr	Gln	Lys	Glu
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Ala	Ile	Gly	Phe	Ala	Thr	Thr	Val	Asp	Arg	Asp	Gly	Arg	Arg	Ser	Val
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A

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 865 870 875 880
 Phe Cys Pro Leu Phe Ala Ser Leu Val Asn Ile Leu Gln Ser Asp Val
 885 890 895
 Met Leu Cys Ile Met Gly Thr Ile Leu Gln Trp Ala Val Glu His Asn
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 Gly Tyr Ala Trp Ser Glu Ser Met Leu Gln Arg Val Leu His Leu Ile
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 Glu His Val Val Thr Phe Thr Phe Thr Gln Lys Ile Ser Lys Pro Gly
 945 950 955 960
 Glu Ala Pro Lys Asn Ser Pro Ser Ile Leu Ala Met Leu Glu Thr Leu
 965 970 975
 Gln Asn Ala Pro Tyr Leu Glu Val His Lys Asp Met Ile Arg Trp Ile
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 Leu Lys Thr Phe Asn Ala Val Lys Lys Met Arg Glu Ser Ser Pro Thr
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 Ser Pro Val Ala Glu Thr Glu Gly Thr Ile Met Glu Glu Ser Ser
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 Ile Gln Asp Pro Glu Lys Tyr Asp Pro Leu Phe Met His Pro Asp
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 Leu Ser Cys Gly Thr His Thr Ser Ser Cys Gly His Ile Met His
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Ser Ala Leu Phe Phe His Tyr Leu Asn Gly Val Pro Ser Pro Pro	1520	1525	1530
Asp Ile Gln Val Pro Gly Thr Ser His Phe Glu His Leu Cys Ser	1535	1540	1545
Tyr Leu Ser Leu Pro Asn Asn Leu Ile Cys Leu Phe Gln Glu Asn	1550	1555	1560
Ser Glu Ile Met Asn Ser Leu Ile Glu Ser Trp Cys Arg Asn Ser	1565	1570	1575
Glu Val Lys Arg Tyr Leu Glu Gly Glu Arg Asp Ala Ile Arg Tyr	1580	1585	1590
Pro Arg Glu Ser Asn Lys Leu Ile Asn Leu Pro Glu Asp Tyr Ser	1595	1600	1605
Ser Leu Ile Asn Gln Ala Ser Asn Phe Ser Cys Pro Lys Ser Gly	1610	1615	1620
Gly Asp Lys Ser Arg Ala Pro Thr Leu Cys Leu Val Cys Gly Ser	1625	1630	1635
Leu Leu Cys Ser Gln Ser Tyr Cys Cys Gln Thr Glu Leu Glu Gly	1640	1645	1650
Glu Asp Val Gly Ala Cys Thr Ala His Thr Tyr Ser Cys Gly Ser	1655	1660	1665
Gly Val Gly Ile Phe Leu Arg Val Arg Glu Cys Gln Val Leu Phe	1670	1675	1680
Leu Ala Gly Lys Thr Lys Gly Cys Phe Tyr Ser Pro Pro Tyr Leu	1685	1690	1695
Asp Asp Tyr Gly Glu Thr Asp Gln Gly Leu Arg Arg Gly Asn Pro	1700	1705	1710
Leu His Leu Cys Lys Glu Arg Phe Lys Lys Ile Gln Lys Leu Trp	1715	1720	1725
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Asn Gln Thr Leu Val Gly Ile Asp Trp Gln His Leu	1745	1750	1755

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 His Leu Cys Gly Arg Val Phe Lys Val Gly Glu Pro Thr Tyr Ser Cys
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 Leu Gly Ser Ile His Arg Asp His Arg Tyr Arg Met Thr Thr Ser Gly
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Ser	Ser	Val	Ala	Ala	His	Gln	Asn	Phe	Gly	Leu	Lys	Ala	Leu	Ser	Trp	305	310	315	320
Leu	Gly	Ser	Val	Ile	Gly	Tyr	Ser	Asp	Gly	Leu	Arg	Arg	Ile	Leu	Cys	325	330	335	
Gln	Val	Gly	Leu	Gln	Glu	Gly	Pro	Asp	Gly	Glu	Asn	Ser	Ser	Leu	Val	340	345	350	
Asp	Arg	Leu	Met	Leu	Asn	Asp	Ser	Lys	Leu	Trp	Lys	Gly	Ala	Arg	Ser	355	360	365	
Val	Tyr	His	Gln	Leu	Phe	Met	Ser	Ser	Leu	Leu	Met	Asp	Leu	Lys	Tyr	370	375	380	
Lys	Lys	Leu	Phe	Ala	Leu	Arg	Phe	Ala	Lys	Asn	Tyr	Arg	Gln	Leu	Gln	385	390	395	400
Arg	Asp	Phe	Met	Glu	Asp	Asp	His	Glu	Arg	Ala	Val	Ser	Val	Thr	Ala	405	410	415	
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Thr	Glu	Glu	Asn	Leu	Met	Thr	Val	Ile	Ile	Lys	Ala	Phe	Met	Asp	His	435	440	445	
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Ala	Leu	Gln	Ala	Phe	Lys	Phe	Arg	Arg	Val	Gln	Ser	Leu	Ile	Leu	Asp	465	470	475	480
Leu	Lys	Tyr	Val	Leu	Ile	Ser	Lys	Pro	Thr	Glu	Trp	Ser	Asp	Glu	Leu	485	490	495	
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Cys	Met	Gln	Gly	Met	Asp	Pro	Ile	Thr	Arg	Gln	Val	Gly	Gln	His	Ile	515	520	525	
Glu	Met	Glu	Pro	Glu	Trp	Glu	Ala	Ala	Phe	Thr	Leu	Gln	Met	Lys	Leu	530	535	540	

Thr	His	Val	Ile	Ser	Met	Val	Gln	Asp	Trp	Cys	Ala	Leu	Asp	Glu	Lys	545	550	555	560
Val	Leu	Ile	Glu	Ala	Tyr	Lys	Lys	Cys	Leu	Ala	Val	Leu	Thr	Gln	Cys	565	570	575	
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Val	Leu	Cys	Ala	Gln	Val	His	Ala	Gly	Met	Trp	Arg	Arg	Asn	Gly	Phe	660	665	670	
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Glu	Met	Phe	Asp	Lys	Asp	Ile	Val	Met	Leu	Gln	Thr	Gly	Val	Ser	Met	690	695	700	
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Tyr	Gln	Leu	Phe	Ser	Thr	Pro	Asp	Tyr	Gly	Lys	Arg	Phe	Ser	Ser	Glu	725	730	735	
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Ser	Arg	Ala	Glu	Gln	Ser	Lys	Ala	Glu	Glu	Ala	Gln	Arg	Lys	Leu	Lys	850	855	860	
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915 920 925
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1235						1240					1245			
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1250						1255					1260			
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1265						1270					1275			
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1280						1285					1290			
Arg	Asn	Pro	Tyr	Ser	Asp	Ser	Ile	Lys	Glu	Met	Leu	Thr	Thr	Phe
1295						1300					1305			
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1310						1315					1320			
Gly	Asp	Pro	Arg	Val	Pro	Ile	Leu	Cys	Trp	Gly	Thr	Cys	Ala	Tyr
1325						1330					1335			
Thr	Ile	Gln	Ser	Ile	Glu	Arg	Ile	Leu	Ser	Asp	Glu	Glu	Lys	Pro
1340						1345					1350			
Val	Phe	Gly	Pro	Leu	Pro	Cys	Arg	Leu	Asp	Asp	Cys	Leu	Arg	Ser
1355						1360					1365			
Leu	Thr	Arg	Phe	Ala	Ala	Ala	His	Trp	Thr	Val	Ala	Leu	Leu	Pro
1370						1375					1380			
Val	Val	Gln	Gly	His	Phe	Cys	Lys	Leu	Phe	Ala	Ser	Leu	Val	Pro
1385						1390					1395			
Ser	Asp	Ser	Tyr	Glu	Asp	Leu	Pro	Cys	Ile	Leu	Asp	Ile	Asp	Met
1400						1405					1410			
Phe	His	Leu	Leu	Val	Gly	Leu	Val	Leu	Ala	Phe	Pro	Ala	Leu	Gln
1415						1420					1425			
Cys	Gln	Asp	Phe	Ser	Gly	Ser	Ser	Leu	Ala	Thr	Gly	Asp	Leu	His
1430						1435					1440			
Ile	Phe	His	Leu	Val	Thr	Met	Ala	His	Ile	Val	Gln	Ile	Leu	Leu
1445						1450					1455			
Thr	Ser	Cys	Thr	Glu	Glu	Asn	Gly	Met	Asp	Gln	Glu	Asn	Pro	Thr
1460						1465					1470			
Gly	Glu	Glu	Glu	Leu	Ala	Ile	Leu	Ser	Leu	His	Lys	Thr	Leu	His
1475						1480					1485			
Gln	Tyr	Thr	Gly	Ser	Ala	Leu	Lys	Glu	Ala	Pro	Ser	Gly	Trp	His
1490						1495					1500			
Leu	Trp	Arg	Ser	Val	Arg	Ala	Ala	Ile	Met	Pro	Phe	Leu	Lys	Cys
1505						1510					1515			

Ser	Ala	Leu	Phe	Phe	His	Tyr	Leu	Asn	Gly	Val	Pro	Ala	Pro	Pro
1520						1525					1530			
Asp	Leu	Gln	Val	Ser	Gly	Thr	Ser	His	Phe	Glu	His	Leu	Cys	Asn
1535						1540					1545			
Tyr	Leu	Ser	Leu	Pro	Thr	Asn	Leu	Ile	His	Leu	Phe	Gln	Glu	Asn
1550						1555					1560			
Ser	Asp	Ile	Met	Asn	Ser	Leu	Ile	Glu	Ser	Trp	Cys	Gln	Asn	Ser
1565						1570					1575			
Glu	Val	Lys	Arg	Tyr	Leu	Asn	Gly	Glu	Arg	Gly	Ala	Ile	Ser	Tyr
1580						1585					1590			
Pro	Arg	Gly	Ala	Asn	Lys	Leu	Ile	Asp	Leu	Pro	Glu	Asp	Tyr	Ser
1595						1600					1605			
Ser	Leu	Ile	Asn	Gln	Ala	Ser	Asn	Phe	Ser	Cys	Pro	Lys	Ser	Gly
1610						1615					1620			
Gly	Asp	Lys	Ser	Arg	Ala	Pro	Thr	Leu	Cys	Leu	Val	Cys	Gly	Ser
1625						1630					1635			
Leu	Leu	Cys	Ser	Gln	Ser	Tyr	Cys	Cys	Gln	Ala	Glu	Leu	Glu	Gly
1640						1645					1650			
Glu	Asp	Val	Gly	Ala	Cys	Thr	Ala	His	Thr	Tyr	Ser	Cys	Gly	Ser
1655						1660					1665			
Gly	Ala	Gly	Ile	Phe	Leu	Arg	Val	Arg	Glu	Cys	Gln	Val	Leu	Phe
1670						1675					1680			
Leu	Ala	Gly	Lys	Thr	Lys	Gly	Cys	Phe	Tyr	Ser	Pro	Pro	Tyr	Leu
1685						1690					1695			
Asp	Asp	Tyr	Gly	Glu	Thr	Asp	Gln	Gly	Leu	Arg	Arg	Gly	Asn	Pro
1700						1705					1710			
Leu	His	Leu	Cys	Gln	Glu	Arg	Phe	Arg	Lys	Ile	Gln	Lys	Leu	Trp
1715						1720					1725			
Gln	Gln	His	Ser	Ile	Thr	Glu	Glu	Ile	Gly	His	Ala	Gln	Glu	Ala
1730						1735					1740			
Asn	Gln	Thr	Leu	Val	Gly	Ile	Asp	Trp	Gln	His	Leu			
1745						1750					1755			

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 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer
 -2282-91

<400> 7
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21

<210> 8
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer -
2385-35

<400> 8
tctcgatatg ttgcagcctt gcta

24

<210> 9
<211> 23
<212> DNA
<213> Artificial sequence

<220>

<223> Description of Artificial Sequence: Primer 2282-94

<400> 9
gtatgaactt gccgaggctt tta

23

<210> 10
<211> 23
<212> DNA
<213> Artificial sequence

<220>

<223> Description of Artificial Sequence: Primer 2294-37

<400> 10
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23

<210> 11
<211> 18
<212> DNA
<213> Artificial sequence

<220>

<223> Description of Artificial Sequence: Primer 2380-88

<400> 11
atggcgtcgc tagagcca

18

<210> 12
<211> 23
<212> DNA
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<220>

<223> Description of Artificial Sequence: Primer 2378-32

<400> 12
caaagcggct gagcatgac atc

23

<210> 13
 <211> 23
 <212> DNA
 <213> Artificial sequence

<220>

<223> Description of Artificial Sequence: Primer 2381-48

<400> 13

tgaacagcca atcacactaa gca

23

<210> 14
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 <212> DNA
 <213> Artificial sequence

<220>

<223> Description of Artificial Sequence: Primer 2385-94

<400> 14

ttataaatgc caaatgccaa

20

<210> 15
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 <212> PRT
 <213> Mouse

<400> 15

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Glu Pro Pro Leu Ala Pro Gln Arg Pro Ala Ser Trp Trp Asp Gln Gln
 20 25 30

Val Asp Phe Tyr Thr Ala Phe Leu His His Leu Ala Gln Leu Val Pro
 35 40 45

Glu Ile Tyr Phe Ala Glu Met Asp Pro Asp Leu Glu Lys Gln Glu Glu
 50 55 60

Ser Val Gln Met Ser Ile Leu Thr Pro Leu Glu Trp Tyr Leu Phe Gly
 65 70 75 80

Glu Asp Pro Asp Ile Cys Leu Glu Lys Leu Lys His Ser Gly Ala Phe
 85 90 95

Gln Leu Cys Gly Lys Val Phe Lys Ser Gly Glu Thr Thr Tyr Ser Cys
 100 105 110

Arg Asp Cys Ala Ile Asp Pro Thr Cys Val Leu Cys Met Asp Cys Phe
 115 120 125

Gln Ser Ser Val His Lys Asn His Arg Tyr Lys Met His Thr Ser Thr
 130 135 140

Gly Gly Gly Phe Cys Asp Cys Gly Asp Thr Glu Ala Trp Lys Thr Gly
 145 150 155 160

Pro Phe Cys Val Asp His Glu Pro Gly Arg Ala Gly Thr Thr Lys Glu
 165 170 175
 Ser Leu His Cys Pro Leu Asn Glu Glu Val Ile Ala Gln Ala Arg Arg
 180 185 190
 Ile Phe Pro Ser Val Ile Lys Tyr Ile Val Glu Met Thr Ile Trp Glu
 195 200 205
 Glu Glu Lys Glu Leu Pro Pro Glu Leu Gln Ile Arg Glu Lys Asn Glu
 210 215 220
 Arg Tyr Tyr Cys Val Leu Phe Asn Asp Glu His His Ser Tyr Asp His
 225 230 235 240
 Val Ile Tyr Ser Leu Gln Arg Ala Leu Asp Cys Glu Leu Ala Glu Ala
 245 250 255
 Gln Leu His Thr Thr Ala Ile Asp Lys Glu Gly Arg Arg Ala Val Lys
 260 265 270
 Ala Gly Val Tyr Ala Thr Cys Gln Glu Ala Lys Glu Asp Ile Lys Ser
 275 280 285
 His Ser Glu Asn Val Ser Gln His Pro Leu His Val Glu Val Leu His
 290 295 300
 Ser Val Val Met Ala His Gln Lys Phe Ala Leu Arg Leu Gly Ser Trp
 305 310 315 320
 Met Asn Lys Ile Met Ser Tyr Ser Ser Asp Phe Arg Gln Ile Phe Cys
 325 330 335
 Gln Ala Cys Leu Val Glu Glu Pro Gly Ser Glu Asn Pro Cys Leu Ile
 340 345 350
 Ser Arg Leu Met Leu Trp Asp Ala Lys Leu Tyr Lys Gly Ala Arg Lys
 355 360 365
 Ile Leu His Glu Leu Ile Phe Ser Ser Phe Phe Met Glu Met Glu Tyr
 370 375 380
 Lys Lys Leu Phe Ala Met Glu Phe Val Lys Tyr Tyr Lys Gln Leu Gln
 385 390 395 400
 Lys Glu Tyr Ile Ser Asp Asp His Glu Arg Ser Ile Ser Ile Thr Ala
 405 410 415
 Leu Ser Val Gln Met Leu Thr Val Pro Thr Leu Ala Arg His Leu Ile
 420 425 430
 Glu Glu Gln Asn Val Ile Ser Val Ile Thr Glu Thr Leu Leu Glu Val
 435 440 445
 Leu Pro Glu Tyr Leu Asp Arg Asn Asn Lys Phe Asn Phe Gln Gly Tyr
 450 455 460
 Ser Gln Asp Lys Leu Gly Arg Val Tyr Ala Val Ile Cys Asp Leu Lys
 465 470 475 480
 Tyr Ile Leu Ile Ser Lys Pro Val Ile Trp Thr Glu Arg Leu Arg Ala
 485 490 495

Gln	Phe	Leu	Glu	Gly	Phe	Arg	Ser	Phe	Leu	Lys	Ile	Leu	Thr	Cys	Met	
			500					505					510			
Gln	Gly	Met	Glu	Glu	Ile	Arg	Arg	Gln	Val	Gly	Gln	His	Ile	Glu	Val	
		515					520					525				
Asp	Pro	Asp	Trp	Glu	Ala	Ala	Ile	Ala	Ile	Gln	Met	Gln	Leu	Lys	Asn	
	530					535					540					
Ile	Leu	Leu	Met	Phe	Gln	Glu	Trp	Cys	Ala	Cys	Asp	Glu	Asp	Leu	Leu	
545					550					555					560	
Leu	Val	Ala	Tyr	Lys	Glu	Cys	His	Lys	Ala	Val	Met	Arg	Cys	Ser	Thr	
			565						570					575		
Asn	Phe	Met	Ser	Ser	Thr	Lys	Thr	Val	Val	Gln	Leu	Cys	Gly	His	Ser	
		580						585					590			
Leu	Glu	Thr	Lys	Ser	Tyr	Lys	Val	Ser	Glu	Asp	Leu	Val	Ser	Ile	His	
		595					600					605				
Leu	Pro	Leu	Ser	Arg	Thr	Leu	Ala	Gly	Leu	His	Val	Arg	Leu	Ser	Arg	
	610					615					620					
Leu	Gly	Ala	Ile	Ser	Arg	Leu	His	Glu	Phe	Val	Pro	Phe	Asp	Ser	Phe	
625					630					635					640	
Gln	Val	Glu	Val	Leu	Val	Glu	Tyr	Pro	Leu	Arg	Cys	Leu	Val	Leu	Val	
			645						650					655		
Ala	Gln	Val	Val	Ala	Glu	Met	Trp	Arg	Arg	Asn	Gly	Leu	Ser	Leu	Ile	
			660					665					670			
Ser	Gln	Val	Phe	Tyr	Tyr	Gln	Asp	Val	Lys	Cys	Arg	Glu	Glu	Met	Tyr	
		675					680					685				
Asp	Lys	Asp	Ile	Ile	Met	Leu	Gln	Ile	Gly	Ala	Ser	Ile	Met	Asp	Pro	
	690					695					700					
Asn	Lys	Phe	Leu	Leu	Leu	Val	Leu	Gln	Arg	Tyr	Glu	Leu	Thr	Asp	Ala	
705					710					715					720	
Phe	Asn	Lys	Thr	Ile	Ser	Thr	Lys	Asp	Gln	Asp	Leu	Ile	Lys	Gln	Tyr	
			725						730					735		
Asn	Thr	Leu	Ile	Glu	Glu	Met	Leu	Gln	Val	Leu	Ile	Tyr	Ile	Val	Gly	
		740						745					750			
Glu	Arg	Tyr	Val	Pro	Gly	Val	Gly	Asn	Val	Thr	Arg	Glu	Glu	Val	Ile	
		755					760					765				
Met	Arg	Glu	Ile	Thr	His	Leu	Leu	Cys	Ile	Glu	Pro	Met	Pro	His	Ser	
	770					775					780					
Ala	Ile	Ala	Arg	Asn	Leu	Pro	Glu	Asn	Glu	Asn	Asn	Glu	Thr	Gly	Leu	
785					790					795					800	
Glu	Asn	Val	Ile	Asn	Lys	Val	Ala	Thr	Phe	Lys	Lys	Pro	Gly	Val	Ser	
			805						810					815		
Gly	His	Gly	Val	Tyr	Glu	Leu	Lys	Asp	Glu	Ser	Leu	Lys	Asp	Phe	Asn	
			820					825					830			

Met Tyr Phe Tyr His Tyr Ser Lys Thr Gln His Ser Lys Ala Glu His
 835 840 845
 Met Gln Lys Lys Arg Arg Lys Gln Glu Asn Lys Asp Glu Ala Leu Pro
 850 855 860
 Pro Pro Pro Pro Pro Glu Phe Cys Pro Ala Phe Ser Lys Val Val Asn
 865 870 875 880
 Leu Leu Ser Cys Asp Val Met Ile Tyr Ile Leu Arg Thr Ile Phe Glu
 885 890 895
 Arg Ala Val Asp Thr Glu Ser Asn Leu Trp Thr Glu Gly Met Leu Gln
 900 905 910
 Met Ala Phe His Ile Leu Ala Leu Gly Leu Leu Glu Glu Lys Gln Gln
 915 920 925
 Leu Gln Lys Ala Pro Glu Glu Glu Val Ala Phe Asp Phe Tyr His Lys
 930 935 940
 Ala Ser Arg Leu Gly Ser Ser Ala Met Asn Ala Gln Asn Ile Gln Met
 945 950 955 960
 Leu Leu Glu Arg Leu Lys Gly Ile Pro Gln Leu Glu Gly Gln Lys Asp
 965 970 975
 Met Ile Thr Trp Ile Leu Gln Met Phe Asp Thr Val Lys Arg Leu Arg
 980 985 990
 Glu Lys Ser Cys Leu Val Val Ala Thr Thr Ser Gly Leu Glu Cys Ile
 995 1000 1005
 Lys Ser Glu Glu Ile Thr His Asp Lys Glu Lys Ala Glu Arg Lys
 1010 1015 1020
 Arg Lys Ala Glu Ala Ala Arg Leu His Arg Gln Lys Ile Met Ala
 1025 1030 1035
 Gln Met Ser Ala Leu Gln Lys Asn Phe Ile Glu Thr His Lys Leu
 1040 1045 1050
 Met Tyr Asp Asn Thr Ser Glu Val Thr Gly Lys Glu Asp Ser Ile
 1055 1060 1065
 Met Glu Glu Glu Ser Thr Ser Ala Val Ser Glu Ala Ser Arg Ile
 1070 1075 1080
 Ala Leu Gly Pro Lys Arg Gly Pro Ala Val Thr Glu Lys Glu Val
 1085 1090 1095
 Leu Thr Cys Ile Leu Cys Gln Glu Glu Gln Glu Val Lys Leu Glu
 1100 1105 1110
 Asn Asn Ala Met Val Leu Ser Ala Cys Val Gln Lys Ser Thr Ala
 1115 1120 1125
 Leu Thr Gln His Arg Gly Lys Pro Val Asp His Leu Gly Glu Thr
 1130 1135 1140
 Leu Asp Pro Leu Phe Met Asp Pro Asp Leu Ala His Gly Thr Tyr
 1145 1150 1155

Thr	Gly	Ser	Cys	Gly	His	Val	Met	His	Ala	Val	Cys	Trp	Gln	Lys
1160						1165					1170			
Tyr	Phe	Glu	Ala	Val	Gln	Leu	Ser	Ser	Gln	Gln	Arg	Ile	His	Val
1175						1180					1185			
Asp	Leu	Phe	Asp	Leu	Glu	Ser	Gly	Glu	Tyr	Leu	Cys	Pro	Leu	Cys
1190						1195					1200			
Lys	Ser	Leu	Cys	Asn	Thr	Val	Ile	Pro	Ile	Ile	Pro	Leu	Gln	Pro
1205						1210					1215			
Gln	Lys	Ile	Asn	Ser	Glu	Asn	Ala	Glu	Ala	Leu	Ala	Gln	Leu	Leu
1220						1225					1230			
Thr	Leu	Ala	Arg	Trp	Ile	Gln	Thr	Val	Leu	Ala	Arg	Ile	Ser	Gly
1235						1240					1245			
Tyr	Asn	Ile	Lys	His	Ala	Lys	Gly	Glu	Ala	Pro	Ala	Val	Pro	Val
1250						1255					1260			
Leu	Phe	Asn	Gln	Gly	Met	Gly	Asp	Ser	Thr	Phe	Glu	Phe	His	Ser
1265						1270					1275			
Ile	Leu	Ser	Phe	Gly	Val	Gln	Ser	Ser	Val	Lys	Tyr	Ser	Asn	Ser
1280						1285					1290			
Ile	Lys	Glu	Met	Val	Ile	Leu	Phe	Ala	Thr	Thr	Ile	Tyr	Arg	Ile
1295						1300					1305			
Gly	Leu	Lys	Val	Pro	Pro	Asp	Glu	Leu	Asp	Pro	Arg	Val	Pro	Met
1310						1315					1320			
Met	Thr	Trp	Ser	Thr	Cys	Ala	Phe	Thr	Ile	Gln	Ala	Ile	Glu	Asn
1325						1330					1335			
Leu	Leu	Gly	Asp	Glu	Gly	Lys	Pro	Leu	Phe	Gly	Ala	Leu	Gln	Asn
1340						1345					1350			
Arg	Gln	His	Ser	Gly	Leu	Lys	Ala	Leu	Met	Gln	Phe	Ala	Val	Ala
1355						1360					1365			
Gln	Arg	Ala	Thr	Cys	Pro	Gln	Val	Leu	Ile	His	Lys	His	Leu	Ala
1370						1375					1380			
Arg	Leu	Leu	Ser	Val	Ile	Leu	Pro	Asn	Leu	Gln	Ser	Glu	Asn	Thr
1385						1390					1395			
Pro	Gly	Leu	Leu	Ser	Val	Asp	Leu	Phe	His	Val	Leu	Val	Gly	Ala
1400						1405					1410			
Val	Leu	Ala	Phe	Pro	Ser	Leu	Tyr	Trp	Asp	Asp	Thr	Val	Asp	Leu
1415						1420					1425			
Gln	Pro	Ser	Pro	Leu	Ser	Ser	Ser	Tyr	Asn	His	Leu	Tyr	Leu	Phe
1430						1435					1440			
His	Leu	Ile	Thr	Met	Ala	His	Met	Leu	Gln	Ile	Leu	Leu	Thr	Thr
1445						1450					1455			
Asp	Thr	Asp	Leu	Ser	Pro	Gly	Pro	Pro	Leu	Ala	Glu	Gly	Glu	Glu
1460						1465					1470			

Asp	Ser	Glu	Glu	Ala	Arg	Cys	Ala	Ser	Ala	Phe	Phe	Val	Glu	Val
1475						1480					1485			
Ser	Gln	His	Thr	Asp	Gly	Leu	Thr	Gly	Cys	Gly	Ala	Pro	Gly	Trp
1490						1495					1500			
Tyr	Leu	Trp	Leu	Ser	Leu	Arg	Asn	Gly	Ile	Thr	Pro	Tyr	Leu	Arg
1505						1510					1515			
Cys	Ala	Ala	Leu	Leu	Phe	His	Tyr	Leu	Leu	Gly	Val	Ala	Pro	Pro
1520						1525					1530			
Glu	Glu	Leu	Phe	Ala	Asn	Ser	Ala	Glu	Gly	Glu	Phe	Ser	Ala	Leu
1535						1540					1545			
Cys	Ser	Tyr	Leu	Ser	Leu	Pro	Thr	Asn	Leu	Phe	Leu	Leu	Phe	Gln
1550						1555					1560			
Glu	Tyr	Trp	Asp	Thr	Ile	Arg	Pro	Leu	Leu	Gln	Arg	Trp	Cys	Gly
1565						1570					1575			
Asp	Pro	Ala	Leu	Leu	Lys	Ser	Leu	Lys	Gln	Lys	Ser	Ala	Val	Val
1580						1585					1590			
Arg	Tyr	Pro	Arg	Lys	Arg	Asn	Ser	Leu	Ile	Glu	Leu	Pro	Glu	Asp
1595						1600					1605			
Tyr	Ser	Cys	Leu	Leu	Asn	Gln	Ala	Ser	His	Phe	Arg	Cys	Pro	Arg
1610						1615					1620			
Ser	Ala	Asp	Asp	Glu	Arg	Lys	His	Pro	Val	Leu	Cys	Leu	Phe	Cys
1625						1630					1635			
Gly	Ala	Ile	Leu	Cys	Ser	Gln	Asn	Ile	Cys	Cys	Gln	Glu	Ile	Val
1640						1645					1650			
Asn	Gly	Glu	Glu	Val	Gly	Ala	Cys	Val	Phe	His	Ala	Leu	His	Cys
1655						1660					1665			
Gly	Ala	Gly	Val	Cys	Ile	Phe	Leu	Lys	Ile	Arg	Glu	Cys	Arg	Val
1670						1675					1680			
Val	Leu	Val	Glu	Gly	Lys	Ala	Arg	Gly	Cys	Ala	Tyr	Pro	Ala	Pro
1685						1690					1695			
Tyr	Leu	Asp	Glu	Tyr	Gly	Glu	Thr	Asp	Pro	Gly	Leu	Lys	Arg	Gly
1700						1705					1710			
Asn	Pro	Leu	His	Leu	Ser	Arg	Glu	Arg	Tyr	Arg	Lys	Leu	His	Leu
1715						1720					1725			
Val	Trp	Gln	Gln	His	Cys	Ile	Ile	Glu	Glu	Ile	Ala	Arg	Ser	Gln
1730						1735					1740			
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<210> 16
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 <212> PRT
 <213> Artificial sequence

155

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<220>
<223> Description of Artificial Sequence: peptide

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1 5 10

<210> 17
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: peptide

<400> 17

Gly Gly Gly Gly Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
1 5 10 15

<210> 18
<211> 5205
<212> DNA
<213> Homo sapiens

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catcatttgg cacaattggt gccagaaatt tactttgctg aaatggaccc agacttggaa 180
aagcaggagg aaagtgtaca aatgtcaata ttcactccac tggaatggta cttatttggg 240
gaagatccag atatttgctt agagaaattg aagcacagtg gagcatttca gctttgtggg 300
agggttttca aaagtggaga gacaacctat tcttgagggg attgtgcaat tgatccaaca 360
tgtgtactct gtatggactg cttccaggac agtgttcata aaaatcatcg ttacaagatg 420
catacttcta ctggaggagg gttctgtgac tgtggagaca cagaggcatg gaaaactggc 480
cctttttgtg taaatcatga acctggaaga gcaggtacta taaaagagaa ttcacgctgt 540
ccgttgaatg aagaggtaat tgtccaagcc aggaaaatat ttccttcagt gataaaatat 600
gtcgtagaaa tgactatatg ggaagaggaa aaagaactgc ctctgaact ccagataagg 660
knryycvndh hsydhgtcat atacagccta caaagagctc ttgactgtga gctcgcagag 720
gcccagttgc ataccactgc cattgacaaa gagggctcgtc gggctgttaa agcgggagct 780

156

A

tatgctgctt gccaggaagc aaaggaagat ataaagagtc attcagaaaa tgtctctcaa	840
catccacttc atgtagaagt attacactca gagattatgg ctcatcagaa atttgctttg	900
cgtcttggtt cctggatgaa caaaattatg agctattcaa gtgacttttag gcagatcttt	960
tgccaagcat gccttagaga agaacctgac tcggagaatc cctgtctcat aagcagggtta	1020
atgctttggg atgcaaagct ttataaaggt gcccgaaga tccttcatga attgatcttc	1080
agcagttttt ttatggagat ggaatacaaa aaactctttg ctatggaatt tgtgaagtat	1140
tataaacaac tgcagaaaga atatatcagt gatgatcatg acagaagtat ctctataact	1200
gcactttcag ttcagatggt tactgttctt actctggctc gacatcttat tgaagagcag	1260
aatgttatct ctgtcattac tgaaactctg ctagaagttt tacctgagta cttggacagg	1320
aacaataaat tcaacttcca gggttatagc caggacaaat tgggaagagt atatgcagta	1380
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aagtcctaca gagtatctga ggatcttgta agcatacatc tgccactctc taggaccctt	1800
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cagattgggtg catctttaat ggatcccaat aagttcttgt tactgggtact tcagagggtat	2100
gaacttgccg aggccttttaa caagaccata tctacaaaag accaggattt gattaaacaa	2160
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gagtacagtg cactctgtag ctatctatct ttacctaaa atttgttctt gctcttccag	4620

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<210> 19
 <211> 1734
 <212> PRT
 <213> Homo sapiens

<400> 19
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 Met Glu Ile Ser Ala Glu Leu Pro Gln Thr Pro Gln Arg Leu Ala Ser
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 Trp Trp Asp Gln Gln Val Asp Phe Tyr Thr Ala Phe Leu His His Leu
 35 40 45
 Ala Gln Leu Val Pro Glu Ile Tyr Phe Ala Glu Met Asp Pro Asp Leu
 50 55 60
 Glu Lys Gln Glu Glu Ser Val Gln Met Ser Ile Phe Thr Pro Leu Glu
 65 70 75 80
 Trp Tyr Leu Phe Gly Glu Asp Pro Asp Ile Cys Leu Glu Lys Leu Lys
 85 90 95
 His Ser Gly Ala Phe Gln Leu Cys Gly Arg Val Phe Lys Ser Gly Glu
 100 105 110
 Thr Thr Tyr Ser Cys Arg Asp Cys Ala Ile Asp Pro Thr Cys Val Leu
 115 120 125
 Cys Met Asp Cys Phe Gln Asp Ser Val His Lys Asn His Arg Tyr Lys
 130 135 140
 Met His Thr Ser Thr Gly Gly Gly Phe Cys Asp Cys Gly Asp Thr Glu
 145 150 155 160
 Ala Trp Lys Thr Gly Pro Phe Cys Val Asn His Glu Pro Gly Arg Ala
 165 170 175
 Gly Thr Ile Lys Glu Asn Ser Arg Cys Pro Leu Asn Glu Glu Val Ile
 180 185 190

Val	Gln	Ala	Arg	Lys	Ile	Phe	Pro	Ser	Val	Ile	Lys	Tyr	Val	Val	Glu	
		195					200					205				
Met	Thr	Ile	Trp	Glu	Glu	Glu	Lys	Glu	Leu	Pro	Pro	Glu	Leu	Gln	Ile	
		210				215					220					
Arg	Glu	Lys	Asn	Glu	Arg	Tyr	Tyr	Cys	Val	Leu	Phe	Asn	Asp	Glu	His	
225					230					235					240	
His	Ser	Tyr	Asp	His	Val	Ile	Tyr	Ser	Leu	Gln	Arg	Ala	Leu	Asp	Cys	
				245					250					255		
Glu	Leu	Ala	Glu	Ala	Gln	Leu	His	Thr	Thr	Ala	Ile	Asp	Lys	Glu	Gly	
			260					265					270			
Arg	Arg	Ala	Val	Lys	Ala	Gly	Ala	Tyr	Ala	Ala	Cys	Gln	Glu	Ala	Lys	
			275				280					285				
Glu	Asp	Ile	Lys	Ser	His	Ser	Glu	Asn	Val	Ser	Gln	His	Pro	Leu	His	
	290					295					300					
Val	Glu	Val	Leu	His	Ser	Glu	Ile	Met	Ala	His	Gln	Lys	Phe	Ala	Leu	
305					310					315					320	
Arg	Leu	Gly	Ser	Trp	Met	Asn	Lys	Ile	Met	Ser	Tyr	Ser	Ser	Asp	Phe	
				325					330					335		
Arg	Gln	Ile	Phe	Cys	Gln	Ala	Cys	Leu	Arg	Glu	Glu	Pro	Asp	Ser	Glu	
			340					345					350			
Asn	Pro	Cys	Leu	Ile	Ser	Arg	Leu	Met	Leu	Trp	Asp	Ala	Lys	Leu	Tyr	
		355					360					365				
Lys	Gly	Ala	Arg	Lys	Ile	Leu	His	Glu	Leu	Ile	Phe	Ser	Ser	Phe	Phe	
	370					375					380					
Met	Glu	Met	Glu	Tyr	Lys	Lys	Leu	Phe	Ala	Met	Glu	Phe	Val	Lys	Tyr	
385					390					395					400	
Tyr	Lys	Gln	Leu	Gln	Lys	Glu	Tyr	Ile	Ser	Asp	Asp	His	Asp	Arg	Ser	
				405					410					415		
Ile	Ser	Ile	Thr	Ala	Leu	Ser	Val	Gln	Met	Phe	Thr	Val	Pro	Thr	Leu	
			420					425					430			
Ala	Arg	His	Leu	Ile	Glu	Glu	Gln	Asn	Val	Ile	Ser	Val	Ile	Thr	Glu	
			435				440					445				
Thr	Leu	Leu	Glu	Val	Leu	Pro	Glu	Tyr	Leu	Asp	Arg	Asn	Asn	Lys	Phe	
			450			455					460					
Asn	Phe	Gln	Gly	Tyr	Ser	Gln	Asp	Lys	Leu	Gly	Arg	Val	Tyr	Ala	Val	
465					470					475					480	
Ile	Cys	Asp	Leu	Lys	Tyr	Ile	Leu	Ile	Ser	Lys	Pro	Thr	Ile	Trp	Thr	
				485					490					495		
Glu	Arg	Leu	Arg	Met	Gln	Phe	Leu	Glu	Gly	Phe	Arg	Ser	Phe	Leu	Lys	
				500				505					510			
Ile	Leu	Thr	Cys	Met	Gln	Gly	Met	Glu	Glu	Ile	Arg	Arg	Gln	Val	Gly	
			515				520					525				

Gln His Ile Glu Val Asp Pro Asp Trp Glu Ala Ala Ile Ala Ile Gln
 530 535 540
 Met Gln Leu Lys Asn Ile Leu Leu Met Phe Gln Glu Trp Cys Ala Cys
 545 550 555 560
 Asp Glu Glu Leu Leu Leu Val Ala Tyr Lys Glu Cys His Lys Ala Val
 565 570 575
 Met Arg Cys Ser Thr Ser Phe Ile Ser Ser Ser Lys Thr Val Val Gln
 580 585 590
 Ser Cys Gly His Ser Leu Glu Thr Lys Ser Tyr Arg Val Ser Glu Asp
 595 600 605
 Leu Val Ser Ile His Leu Pro Leu Ser Arg Thr Leu Ala Gly Leu His
 610 615 620
 Val Arg Leu Ser Arg Leu Gly Ala Val Ser Arg Leu His Glu Phe Val
 625 630 635 640
 Ser Phe Glu Asp Phe Gln Val Glu Val Leu Val Glu Tyr Pro Leu Arg
 645 650 655
 Cys Leu Val Leu Val Ala Gln Val Val Ala Glu Met Trp Arg Arg Asn
 660 665 670
 Gly Leu Ser Leu Ile Ser Gln Val Phe Tyr Tyr Gln Asp Val Lys Cys
 675 680 685
 Arg Glu Glu Met Tyr Asp Lys Asp Ile Ile Met Leu Gln Ile Gly Ala
 690 695 700
 Ser Leu Met Asp Pro Asn Lys Phe Leu Leu Leu Val Leu Gln Arg Tyr
 705 710 715 720
 Glu Leu Ala Glu Ala Phe Asn Lys Thr Ile Ser Thr Lys Asp Gln Asp
 725 730 735
 Leu Ile Lys Gln Tyr Asn Thr Leu Ile Glu Glu Met Leu Gln Val Leu
 740 745 750
 Ile Tyr Ile Val Gly Glu Arg Tyr Val Pro Gly Val Gly Asn Val Thr
 755 760 765
 Lys Glu Glu Val Thr Met Arg Glu Ile Ile His Leu Leu Cys Ile Glu
 770 775 780
 Pro Met Pro His Ser Ala Ile Ala Lys Asn Leu Pro Glu Asn Glu Asn
 785 790 795 800
 Asn Glu Thr Gly Leu Glu Asn Val Ile Asn Lys Val Ala Thr Phe Lys
 805 810 815
 Lys Pro Gly Val Ser Gly His Gly Val Tyr Glu Leu Lys Asp Glu Ser
 820 825 830
 Leu Lys Asp Phe Asn Met Tyr Phe Tyr His Tyr Ser Lys Thr Gln His
 835 840 845
 Ser Lys Ala Glu His Met Gln Lys Lys Arg Arg Lys Gln Glu Asn Lys
 850 855 860

Asp	Glu	Ala	Leu	Pro	Pro	Pro	Pro	Pro	Pro	Glu	Phe	Cys	Pro	Ala	Phe	865	870	875	880
Ser	Lys	Val	Ile	Asn	Leu	Leu	Asn	Cys	Asp	Ile	Met	Met	Tyr	Ile	Leu	885	890	895	
Arg	Thr	Val	Phe	Glu	Arg	Ala	Ile	Asp	Thr	Asp	Ser	Asn	Leu	Trp	Thr	900	905	910	
Glu	Gly	Met	Leu	Gln	Met	Ala	Phe	His	Ile	Leu	Ala	Leu	Gly	Leu	Leu	915	920	925	
Glu	Glu	Lys	Gln	Gln	Leu	Gln	Lys	Ala	Pro	Glu	Glu	Glu	Val	Thr	Phe	930	935	940	
Asp	Phe	Tyr	His	Lys	Ala	Ser	Arg	Leu	Gly	Ser	Ser	Ala	Met	Asn	Ile	945	950	955	960
Gln	Met	Leu	Leu	Glu	Lys	Leu	Lys	Gly	Ile	Pro	Gln	Leu	Glu	Gly	Gln	965	970	975	
Lys	Asp	Met	Ile	Thr	Trp	Ile	Leu	Gln	Met	Phe	Asp	Thr	Val	Lys	Arg	980	985	990	
Leu	Arg	Glu	Lys	Ser	Cys	Leu	Ile	Val	Ala	Thr	Thr	Ser	Gly	Ser	Glu	995	1000	1005	
Ser	Ile	Lys	Asn	Asp	Glu	Ile	Thr	His	Asp	Lys	Glu	Lys	Ala	Glu		1010	1015	1020	
Arg	Lys	Arg	Lys	Ala	Glu	Ala	Ala	Arg	Leu	His	Arg	Gln	Lys	Ile		1025	1030	1035	
Met	Ala	Gln	Met	Ser	Ala	Leu	Gln	Lys	Asn	Phe	Ile	Glu	Thr	His		1040	1045	1050	
Lys	Leu	Met	Tyr	Asp	Asn	Thr	Ser	Glu	Met	Pro	Gly	Lys	Glu	Asp		1055	1060	1065	
Ser	Ile	Met	Glu	Glu	Glu	Ser	Thr	Pro	Ala	Val	Ser	Asp	Tyr	Ser		1070	1075	1080	
Arg	Ile	Ala	Leu	Gly	Pro	Lys	Arg	Gly	Pro	Ser	Val	Thr	Glu	Lys		1085	1090	1095	
Glu	Val	Leu	Thr	Cys	Ile	Leu	Cys	Gln	Glu	Glu	Gln	Glu	Val	Lys		1100	1105	1110	
Ile	Glu	Asn	Asn	Ala	Met	Val	Leu	Ser	Ala	Cys	Val	Gln	Lys	Ser		1115	1120	1125	
Thr	Ala	Leu	Thr	Gln	His	Arg	Gly	Lys	Pro	Ile	Glu	Leu	Ser	Gly		1130	1135	1140	
Glu	Ala	Leu	Asp	Pro	Leu	Phe	Met	Asp	Pro	Asp	Leu	Ala	Tyr	Gly		1145	1150	1155	
Thr	Tyr	Thr	Gly	Ser	Cys	Gly	His	Val	Met	His	Ala	Val	Cys	Trp		1160	1165	1170	
Gln	Lys	Tyr	Phe	Glu	Ala	Val	Gln	Leu	Ser	Ser	Gln	Gln	Arg	Ile		1175	1180	1185	

His Val Asp Leu Phe Asp Leu Glu Ser Gly Glu Tyr Leu Cys Pro	1190	1195	1200
Leu Cys Lys Ser Leu Cys Asn Thr Val Ile Pro Ile Ile Pro Leu	1205	1210	1215
Gln Pro Gln Lys Ile Asn Ser Glu Asn Ala Asp Ala Leu Ala Gln	1220	1225	1230
Leu Leu Thr Leu Ala Arg Trp Ile Gln Thr Val Leu Ala Arg Ile	1235	1240	1245
Ser Gly Tyr Asn Ile Arg His Ala Lys Gly Glu Asn Pro Ile Pro	1250	1255	1260
Ile Phe Phe Asn Gln Gly Met Gly Asp Ser Thr Leu Glu Phe His	1265	1270	1275
Ser Ile Leu Ser Phe Gly Val Glu Ser Ser Ile Lys Tyr Ser Asn	1280	1285	1290
Ser Ile Lys Glu Met Val Ile Leu Phe Ala Thr Thr Ile Tyr Arg	1295	1300	1305
Ile Gly Leu Lys Val Pro Pro Asp Glu Arg Asp Pro Arg Val Pro	1310	1315	1320
Met Leu Thr Trp Ser Thr Cys Ala Phe Thr Ile Gln Ala Ile Glu	1325	1330	1335
Asn Leu Leu Gly Asp Glu Gly Lys Pro Leu Phe Gly Ala Leu Gln	1340	1345	1350
Asn Arg Gln His Asn Gly Leu Lys Ala Leu Met Gln Phe Ala Val	1355	1360	1365
Ala Gln Arg Ile Thr Cys Pro Gln Val Leu Ile Gln Lys His Leu	1370	1375	1380
Val Arg Leu Leu Ser Val Val Leu Pro Asn Ile Lys Ser Glu Asp	1385	1390	1395
Thr Pro Cys Leu Leu Ser Ile Asp Leu Phe His Val Leu Val Gly	1400	1405	1410
Ala Val Leu Ala Phe Pro Ser Leu Tyr Trp Asp Asp Pro Val Asp	1415	1420	1425
Leu Gln Pro Ser Ser Val Ser Ser Ser Tyr Asn His Leu Tyr Leu	1430	1435	1440
Phe His Leu Ile Thr Met Ala His Met Leu Gln Ile Leu Leu Thr	1445	1450	1455
Val Asp Thr Gly Leu Pro Leu Ala Gln Val Gln Glu Asp Ser Glu	1460	1465	1470
Glu Ala His Ser Ala Ser Ser Phe Phe Ala Glu Ile Ser Gln Tyr	1475	1480	1485
Thr Ser Gly Ser Ile Gly Cys Asp Ile Pro Gly Trp Tyr Leu Trp	1490	1495	1500

Val	Ser	Leu	Lys	Asn	Gly	Ile	Thr	Pro	Tyr	Leu	Arg	Cys	Ala	Ala
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Leu	Phe	Phe	His	Tyr	Leu	Leu	Gly	Val	Thr	Pro	Pro	Glu	Glu	Leu
1520						1525					1530			
His	Thr	Asn	Ser	Ala	Glu	Gly	Glu	Tyr	Ser	Ala	Leu	Cys	Ser	Tyr
1535						1540					1545			
Leu	Ser	Leu	Pro	Thr	Asn	Leu	Phe	Leu	Leu	Phe	Gln	Glu	Tyr	Trp
1550						1555					1560			
Asp	Thr	Val	Arg	Pro	Leu	Leu	Gln	Arg	Arg	Cys	Ala	Asp	Pro	Ala
1565						1570					1575			
Leu	Leu	Asn	Cys	Leu	Lys	Gln	Lys	Asn	Thr	Val	Val	Arg	Tyr	Pro
1580						1585					1590			
Arg	Lys	Arg	Asn	Ser	Leu	Ile	Glu	Leu	Pro	Asp	Asp	Tyr	Ser	Cys
1595						1600					1605			
Leu	Leu	Asn	Gln	Ala	Ser	His	Phe	Arg	Cys	Pro	Arg	Ser	Ala	Asp
1610						1615					1620			
Asp	Glu	Arg	Lys	His	Pro	Val	Leu	Cys	Leu	Phe	Cys	Gly	Ala	Ile
1625						1630					1635			
Leu	Cys	Ser	Gln	Asn	Ile	Cys	Cys	Gln	Glu	Ile	Val	Asn	Gly	Glu
1640						1645					1650			
Glu	Val	Gly	Ala	Cys	Ile	Phe	His	Ala	Leu	His	Cys	Lys	Ala	Arg
1655						1660					1665			
Gly	Cys	Ala	Tyr	Pro	Ala	Pro	Tyr	Leu	Asp	Glu	Tyr	Gly	Glu	Thr
1670						1675					1680			
Asp	Pro	Gly	Leu	Lys	Arg	Gly	Asn	Pro	Leu	His	Leu	Ser	Arg	Glu
1685						1690					1695			
Arg	Tyr	Arg	Lys	Leu	His	Leu	Val	Trp	Gln	Gln	His	Cys	Ile	Ile
1700						1705					1710			
Glu	Glu	Ile	Ala	Arg	Ser	Gln	Glu	Thr	Asn	Gln	Met	Leu	Phe	Gly
1715						1720					1725			
Phe	Asn	Trp	Gln	Leu	Leu									
1730														

<210> 20
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 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of Artificial Sequence: PCR Primer

<400> 20
 agaaggagag tacagtgcac tc

22

<210> 21
 <211> 20

<212> DNA
 <213> Artificial sequence

 <220>
 <223> Description of Artificial Sequence: PCR Primer

 <400> 21
 cgaaagcatc ctgtcctctg 20

 <210> 22
 <211> 18
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Description of Artificial Sequence: PCR Primer

 <400> 22
 aggaagctgt gggtcatgt 18

 <210> 23
 <211> 14
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Description of Artificial Sequence: PCR Primer

 <400> 23
 gtttaggaaga actg 14

 <210> 24
 <211> 20
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Description of Artificial Sequence: PCR Primer

 <400> 24
 aagaacagcg aaggcaacag 20

 <210> 25
 <211> 22
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Description of Artificial Sequence: PCR Primer

 <400> 25
 cgcagctacc ccaacacatt ct 22

 <210> 26
 <211> 22

165

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<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

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22

<210> 27
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

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caaaacttta taaaggtgcc cgtaa

25

<210> 28
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 28
attccctgca tgcacttcag taa

23

<210> 29
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 29
cattccctgc atgcatttca g

21